

SEQUENCE LISTING

<110> Ajinomoto Co. Inc.

<120>

<130> OP1628

<150> JP 2002-336340

<151> 2002-11-20

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 1

agggaattcc ccgttctgga taatgttttt tgcgccgac

39

<210> 2

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 2

cggatgcatc tagagttaac ctgcagggtg aaattgttat ccgtcacaa ttccacac 58

<210> 3

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 3

tgacctgcag gtttgcacag aggatggccc atgtt 35

<210> 4

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 4

cattctagat ccctaaactt tacagcaaac cgcat 36

<210> 5

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

catttcctgc aggcaaagga gatgagcgta atggtgatca tggaaatctt cattacaggt 60
ctgc 64

<210> 6

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

gggcgagcta gaagagctcc aaaacccgcg aaaactaacc catcaacatc 50

<210> 7

<211> 711

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1).. (711)

<400> 7

atg gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt	48
Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser	
1 5 10 15	
ctt tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga	96
Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly	
20 25 30	
att aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct	144
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser	
35 40 45	
gac gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc	192
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser	
50 55 60	
aat gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct	240
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala	
65 70 75 80	
tac ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac	288
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn	
85 90 95	
aag gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc	336
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro	
100 105 110	
gat gac acg cct ttg ggc ggt tcg gcg gtg gcc act gac acg cgc aac	384
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn	
115 120 125	
cgg gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag	432
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys	
130 135 140	
ccc atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat	480
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr	
145 150 155 160	
ttg gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac	528
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp	
165 170 175	
acc gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gca agc ctg atc	576
Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile	
180 185 190	
tgg ttc ccg ctg gtg ggt ttc ggc gca gca gca ttg tca cgc ccg ctg	624
Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu	
195 200 205	
tcc agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg	672
Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val	
210 215 220	
atg acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag	711
Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly	

225

230

235

<210> 8

<211> 236

<212> PRT

<213> Brevibacterium lactofermentum

<400> 8

```

Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
  1           5           10           15
Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
      20           25           30
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
      35           40           45
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
      50           55           60
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
      65           70           75           80
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
      85           90           95
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
      100          105          110
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn
      115          120          125
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys
      130          135          140
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr
      145          150          155          160
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
      165          170          175
Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile
      180          185          190
Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu
      195          200          205
Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val
      210          215          220
Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
225           230           235

```

<210> 9

<211> 712

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1).. (375)

<400> 9

```
atg gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt 48
Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
  1           5           10          15
ctt ttg ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga 96
Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
      20           25           30
att aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct 144
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
      35           40           45
gac gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc 192
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
      50           55           60
aat gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct 240
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
      65           70           75           80
tac ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac 288
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
      85           90           95
aag gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc 336
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
      100          105          110
gat gac acg cct ttg ggc gtg ttc ggc ggt ggc cac tga cacgcgcaac 385
Asp Asp Thr Pro Leu Gly Val Phe Gly Gly Gly His
      115          120          125
cgggtgcggg tggaggtgag cgtcgataag cagcgggttt ggggtgaagcc catgttgatg 445
gcaatcgtgc tgacctggtt gaaccggaat gcgtatttgg acgcgtttgt gtttatcggc 505
ggcgtcggcg cgcaatacgg cgacaccgga cgggtggattt tcgccgtgg cgcgttcgcg 565
gcaagcctga tctggttccc gctggtgggt ttccggcgag cagcattgtc acgcccgtg 625
tccagcccca aggtgtggcg ctggatcaac gtcgtcgtgg cagttgtgat gaccgcattg 685
gccatcaaac tgatgttgat gggttag 712
```

<210> 10

<211> 124

<212> PRT

<213> Brevibacterium lactofermentum

<400> 10

```
Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
  1           5           10          15
Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
      20           25           30
```

Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
 35 40 45
 Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
 50 55 60
 Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
 65 70 75 80
 Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
 85 90 95
 Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
 100 105 110
 Asp Asp Thr Pro Leu Gly Val Phe Gly Gly Gly His
 115 120

<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

aaagaattcg cacggtcac tgtattcggc tgcaacttt 39

<210> 12

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 12

aaagaattcg ccgtgttgct aggatggttg ttcttgatc a 41

<210> 13

<211> 1197

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (272)..(1153)

<400> 13

```

ccaggcgact gtcttcaata ttacagccgc aactactgac atgacgggtg atggtgttca 60
caattccaag gcgatcgcca cccaacgcag tgatcaccag ataatgtgtt gcgatgacag 120
tgtcaaaactg gttattcctt taaggggtga gttgttctta aggaaagcat aaaaaaaca 180
tgcatacaac aatcagaacg gttctgtctg cttgctttta atgccatacc aaacgtacca 240
ttgagacact tgtttgcaca gaggatggcc c atg ttc acg gga agt att gtc 292
                                Met Phe Thr Gly Ser Ile Val
                                1         5
gcg att gtt act ccg atg gat gaa aaa ggt aat gtc tgt cgg gct agc 340
Ala Ile Val Thr Pro Met Asp Glu Lys Gly Asn Val Cys Arg Ala Ser
        10         15         20
ttg aaa aaa ctg att gat tat cat gtc gcc agc ggt act tcg gcg atc 388
Leu Lys Lys Leu Ile Asp Tyr His Val Ala Ser Gly Thr Ser Ala Ile
        25         30         35
gtt tct gtt ggc acc act ggc gag tcc gct acc tta aat cat gac gaa 436
Val Ser Val Gly Thr Thr Gly Glu Ser Ala Thr Leu Asn His Asp Glu
        40         45         50         55
cat gct gat gtg gtg atg atg acg ctg gat ctg gct gat ggg cgc att 484
His Ala Asp Val Val Met Met Thr Leu Asp Leu Ala Asp Gly Arg Ile
        60         65         70
ccg gta att gcc ggg acc ggc gct aac gct act gcg gaa gcc att agc 532
Pro Val Ile Ala Gly Thr Gly Ala Asn Ala Thr Ala Glu Ala Ile Ser
        75         80         85
ctg acg cag cgc ttc aat gac agt ggt atc gtc ggc tgc ctg acg gta 580
Leu Thr Gln Arg Phe Asn Asp Ser Gly Ile Val Gly Cys Leu Thr Val
        90         95         100
acc cct tac tac aat cgt ccg tcg caa gaa ggt ttg tat cag cat ttc 628
Thr Pro Tyr Tyr Asn Arg Pro Ser Gln Glu Gly Leu Tyr Gln His Phe
        105        110        115
aaa gcc atc gct gag cat act gac ctg ccg caa att ctg tat aat gtg 676
Lys Ala Ile Ala Glu His Thr Asp Leu Pro Gln Ile Leu Tyr Asn Val
        120        125        130        135
ccg tcc cgt act ggc tgc gat ctg ctc ccg gaa acg gtg ggc cgt ctg 724
Pro Ser Arg Thr Gly Cys Asp Leu Leu Pro Glu Thr Val Gly Arg Leu
        140        145        150
gcg aaa gta aaa aat att atc gga atc aaa gag gca aca ggg aac tta 772
Ala Lys Val Lys Asn Ile Ile Gly Ile Lys Glu Ala Thr Gly Asn Leu
        155        160        165
acg cgt gta aac cag atc aaa gag ctg gtt tca gat gat ttt gtt ctg 820
Thr Arg Val Asn Gln Ile Lys Glu Leu Val Ser Asp Asp Phe Val Leu
        170        175        180
ctg agc ggc gat gat gcg agc gcg ctg gac ttc atg caa ttg ggc ggt 868
Leu Ser Gly Asp Asp Ala Ser Ala Leu Asp Phe Met Gln Leu Gly Gly
        185        190        195

```

cat ggg gtt att tcc gtt acg act aac gtc gca gcg cgt gat atg gcc	916
His Gly Val Ile Ser Val Thr Thr Asn Val Ala Ala Arg Asp Met Ala	
200 205 210 215	
cag atg tgc aaa ctg gca gca gaa gaa cat ttt gcc gag gca cgc gtt	964
Gln Met Cys Lys Leu Ala Ala Glu Glu His Phe Ala Glu Ala Arg Val	
220 225 230	
att aat cag cgt ctg atg cca tta cac aac aaa cta ttt gtc gaa ccc	1012
Ile Asn Gln Arg Leu Met Pro Leu His Asn Lys Leu Phe Val Glu Pro	
235 240 245	
aat cca atc ccg gtg aaa tgg gca tgt aag gaa ctg ggt ctt gtg gcg	1060
Asn Pro Ile Pro Val Lys Trp Ala Cys Lys Glu Leu Gly Leu Val Ala	
250 255 260	
acc gat acg ctg cgc ctg cca atg aca cca atc acc gac agt ggt cgt	1108
Thr Asp Thr Leu Arg Leu Pro Met Thr Pro Ile Thr Asp Ser Gly Arg	
265 270 275	
gag acg gtc aga gcg gcg ctt aag cat gcc ggt ttg ctg taa	1150
Glu Thr Val Arg Ala Ala Leu Lys His Ala Gly Leu Leu	
280 285 290	
agtttaggga gatttgatgg cttactctgt tcaaaagtgc gcgctgg	1197

<400> 14

Met	Phe	Thr	Gly	Ser	Ile	Val	Ala	Ile	Val	Thr	Pro	Met	Asp	Glu	Lys
1				5					10					15	
Gly	Asn	Val	Cys	Arg	Ala	Ser	Leu	Lys	Lys	Leu	Ile	Asp	Tyr	His	Val
			20					25					30		
Ala	Ser	Gly	Thr	Ser	Ala	Ile	Val	Ser	Val	Gly	Thr	Thr	Gly	Glu	Ser
		35					40					45			
Ala	Thr	Leu	Asn	His	Asp	Glu	His	Ala	Asp	Val	Val	Met	Met	Thr	Leu
	50					55					60				
Asp	Leu	Ala	Asp	Gly	Arg	Ile	Pro	Val	Ile	Ala	Gly	Thr	Gly	Ala	Asn
65					70					75					80
Ala	Thr	Ala	Glu	Ala	Ile	Ser	Leu	Thr	Gln	Arg	Phe	Asn	Asp	Ser	Gly
				85					90					95	
Ile	Val	Gly	Cys	Leu	Thr	Val	Thr	Pro	Tyr	Tyr	Asn	Arg	Pro	Ser	Gln
			100					105					110		
Glu	Gly	Leu	Tyr	Gln	His	Phe	Lys	Ala	Ile	Ala	Glu	His	Thr	Asp	Leu
	115						120				125				
Pro	Gln	Ile	Leu	Tyr	Asn	Val	Pro	Ser	Arg	Thr	Gly	Cys	Asp	Leu	Leu
	130					135					140				
Pro	Glu	Thr	Val	Gly	Arg	Leu	Ala	Lys	Val	Lys	Asn	Ile	Ile	Gly	Ile

145		150		155		160									
Lys	Glu	Ala	Thr	Gly	Asn	Leu	Thr	Arg	Val	Asn	Gln	Ile	Lys	Glu	Leu
				165					170					175	
Val	Ser	Asp	Asp	Phe	Val	Leu	Leu	Ser	Gly	Asp	Asp	Ala	Ser	Ala	Leu
			180						185					190	
Asp	Phe	Met	Gln	Leu	Gly	Gly	His	Gly	Val	Ile	Ser	Val	Thr	Thr	Asn
		195					200					205			
Val	Ala	Ala	Arg	Asp	Met	Ala	Gln	Met	Cys	Lys	Leu	Ala	Ala	Glu	Glu
	210					215					220				
His	Phe	Ala	Glu	Ala	Arg	Val	Ile	Asn	Gln	Arg	Leu	Met	Pro	Leu	His
225					230					235				240	
Asn	Lys	Leu	Phe	Val	Glu	Pro	Asn	Pro	Ile	Pro	Val	Lys	Trp	Ala	Cys
			245						250				255		
Lys	Glu	Leu	Gly	Leu	Val	Ala	Thr	Asp	Thr	Leu	Arg	Leu	Pro	Met	Thr
			260					265					270		
Pro	Ile	Thr	Asp	Ser	Gly	Arg	Glu	Thr	Val	Arg	Ala	Ala	Leu	Lys	His
		275					280					285			
Ala	Gly	Leu	Leu												
		290													